SEQUENCE LISTING

	, , ,	CEMBERT	INFORMATION:
1	(T)	GENERAL	THEORWALLON:

- (i) APPLICANTS: Henry A. Lester, Norman Davidson, Paulo Kofuji
- (ii) TITLE OF INVENTION: Inward Rectifier, G-Protein Activated, Mammalian, Potassium Channels and Uses Thereof
 - (iii) NUMBER OF SEQUENCES: 2
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 - (B) STREET: 4 Embarcadero Center, Suite 3400
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-4187
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US (B) FILING DATE:

 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Trecartin, Richard F.
 - (B) REGISTRATION NUMBER: 31,801
 - (C) REFERENCE/DOCKET NUMBER: A63098/RFT
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 781-1989
 - (B) TELEFAX: (415) 398-3249
 - (C) TELEX: 910 277299
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2076 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:

25

- (A) NAME/KEY: CDS
- (B) LOCATION: 32..1534
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA	TCTGGATCTC	CCCTCCGTAT	T	ATG Met	TCT Ser	GCA Ala	CTC Leu	CGA Arg	AGG Arg	AAA Lys	52
		•		1				5			

TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC 100 Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly 10 15

148 Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro 30



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AAG Lys 40	AAG Lys	AAA Lys	CGG Arg	CAG Gln	CGG Arg 45	TTC Phe	GTG Val	GAC Asp	AAG Lys	AAC Asn 50	GGT Gly	CGG Arg	Cys	AAT Asn	GTG Val 55	196
CAG Gln	CAC His	GGC Gly	AAC Asn	CTG Leu 60	GGC Gly	AGC Ser	GAG Glu	ACC Thr	AGT Ser 65	CGC Arg	TAC Tyr	CTT Leu	TCC Ser	GAC Asp 70	CTC Leu	. 244
TTC Phe	ACT Thr	ACC Thr	CTG Leu 75	GTG Val	GAT Asp	CTC Leu	AAG Lys	TGG Trp 80	CGT Arg	TGG Trp	AAC Asn	CTC Leu	TTT Phe 85	ATC Ile	TTC Phe	292
ATC Ile	CTC Leu	ACC Thr 90	TAC Tyr	ACC Thr	GTG Val	GCC Ala	TGG Trp 95	CTC Leu	TTC Phe	ATG Met	GCG Ala	TCC Ser 100	ATG Met	TGG Trp	TGG Trp	340
GTG Val	ATC Ile 105	GCT Ala	TAT Tyr	ACC Thr	CGG Arg	GGC Gly 110	GAC Asp	CTG Leu	AAC Asn	AAA Lys	GCC Ala 115	CAT His	GTC Val	GGC Gly	AAC Asn	388
TAC Tyr 120	ACT Thr	CCC Pro	TGT Cys	GTG Val	GCC Ala 125	AAT Asn	GTC Val	TAT Tyr	AAC Asn	TTC Phe 130	CCC Pro	TCT Ser	GCC Ala	TTC Phe	CTT Leu 135	436
TTC Phe	TTC Phe	ATC Ile	GAG Glu	ACC Thr 140	GAG Glu	GCC Ala	ACC Thr	ATC Ile	GGC Gly 145	TAT Tyr	GGC Gly	TAC Tyr	CGC Arg	TAC Tyr 150	ATC Ile	484
ACC Thr	GAC Asp	AAG Lys	TGC Cys 155	CCC Pro	GAG Glu	GGC Gly	ATC Ile	ATC Ile 160	CTT Leu	TTC Phe	CTT Leu	TTC Phe	CAG Gln 165	TCC Ser	ATC Ile	532
CTT Leu	GGC Gly	TCC Ser 170	ATC Ile	GTG Val	GAC Asp	GCT Ala	TTC Phe 175	CTC Leu	ATC Ile	GGC Gly	TGC Cys	ATG Met 180	TTC Phe	ATC Ile	AAG Lys	580
ATG Met	TCC Ser 185	CAG Gln	CCC Pro	AAA Lys	AAG Lys	CGC Arg 190	GCC Ala	GAG Glu	ACC Thr	CTC Leu	ATG Met 195	TTT Phe	AGC Ser	GAG Glu	CAT His	628
GCG Ala 200	Val	ATT Ile	TCC Ser	ATG Met	AGG Arg 205	GAC Asp	GGA Gly	AAA Lys	CTC Leu	ACT Thr 210	CTC Leu	ATG Met	TTC Phe	CGG Arg	GTG Val 215	676
GGC Gly	AAC Asn	CTG Leu	CGC Arg	AAC Asn 220	Ser	CAC His	ATG Met	GTC Val	TCC Ser 225	GCG Ala	CAG Gln	ATC Ile	CGC Arg	TGC Cys 230	Lys	724
CTG Leu	CTC Leu	AAA Lys	TCT Ser 235	CGG Arg	CAG Gln	ACA Thr	CCT Pro	GAG Glu 240	Gly	GAG Glu	TTT Phe	CTA Leu	CCC Pro 245	CTT Leu	GAC Asp	772
CAA Gln	CTT	GAA Glu 250	Leu	GAT Asp	GTA Val	GGT Gly	TTT Phe 255	Ser	ACA Thr	GGG Gly	GCA Ala	GAT Asp 260	Gln	CTT Leu	TTT Phe	820
CTT Leu	GTG Val 265	Ser	CCT Pro	CTC Leu	ACC Thr	ATT Ile 270	Cys	CAC His	GTG Val	ATC	GAT Asp 275	Ala	AAA Lys	AGC Ser	CCC Pro	868
TTT Phe 280	Tyr	GAC	CTA Leu	TCC	Gln 285	Arg	AGC Ser	ATG Met	CAA Gln	ACT Thr 290	Glu	CAG Gln	TTC Phe	GAG Glu	GTG Val 295	916
GTC Val	GTC Val	ATC Ile	CTG Leu	GAA Glu 300	Gly	ATC Ile	GTG Val	GAA Glu	ACC Thr 305	Thr	GGG Gly	ATG Met	ACT Thr	TGT Cys 310	CAA Gln	964

GCT Ala	CGA Arg	ACA Thr	TCA Ser 315	TAC Tyr	ACC Thr	GAA Glu	GAT Asp	GAA Glu 320	GTT Val	CTT Leu	TGG Trp	GGT Gly	CAT His 325	CGT Arg	TTT Phe	1012
TTC Phe	CCT Pro	GTA Val 330	ATT Ile	TCT Ser	TTA Leu	GAA Glu	GAA Glu 335	GGA Gly	TTC Phe	TTT Phe	AAA Lys	GTC Val 340	GAT Asp	TAC Tyr	TCC Ser	1060
CAG Gln	TTC Phe 345	CAT His	GCA Ala	ACC Thr	TTT Phe	GAA Glu 350	GTC Val	CCC Pro	ACC Thr	CCT Pro	CCG Pro 355	TAC Tyr	AGT Ser	GTG Val	TÀ2 TÀ2	1108
GAG Glu 360	CAG Gln	GAA Glu	GAA Glu	ATG Met	CTT Leu 365	CTC Leu	ATG Met	TCT Ser	TCC Ser	CCT Pro 370	TTA Leu	ATA Ile	GCA Ala	CCA Pro	GCC Ala 375	1156
ATA Ile	ACC Thr	AAC Asn	AGC Ser	AAA Lys 380	GAA Glu	AGA Arg	CAC His	AAT Asn	TCT Ser 385	GTG Val	GAG Glu	TGC	TTA Leu	GAT Asp 390	GGA Gly	1204
CTA Leu	GAT Asp	GAC Asp	ATT Ile 395	AGC Ser	ACA Thr	AAA Lys	CTT Leu	CCA Pro 400	TCG Ser	AAG Lys	CTG Leu	CAG Gln	AAA Lys 405	ATT Ile	ACG Thr	1252
GGG Gly	AGA Arg	GAA Glu 410	GAC Asp	TTT Phe	CCC Pro	AAA Lys	AAA Lys 415	CTC Leu	CTG Leu	AGG Arg	ATG Met	AGT Ser 420	TCT Ser	ACA Thr	ACT Thr	1300
TCA Ser	GAA Glu 425	AAA Lys	GCC Ala	TAT Tyr	AGT Ser	TTG Leu 430	GGT Gly	GAT Asp	TTG Leu	CCC Pro	ATG Met 435	AAA Lys	CTC Leu	CAA Gln	CGA Arg	1348
ATA Ile 440	Ser	TCG Ser	GTT Val	CCT Pro	GGC Gly 445	AAC Asn	TCT Ser	GAA Glu	GAA Glu	AAA Lys 450	CTG Leu	GTA Val	TCT Ser	AAA Lys	ACC Thr 455	1396
ACC Thr	AAG Lys	ATG Met	TTA Leu	TCA Ser 460	GAT Asp	CCC Pro	ATG Met	AGC Ser	CAG Gln 465	TCT Ser	GTG Val	GCC Ala	GAT	TTG Leu 470	CCA Pro	1444
CCG Pro	AAG Lys	CTT Leu	CAA Gln 475	AAG Lys	ATG Met	GCT Ala	GGA Gly	GGA Gly 480	Pro	ACC Thr	AGG Arg	ATG Met	GAA Glu 485	GGG Gly	AAT Asn	1492
CTT Leu	CCA Pro	GCC Ala 490	AAA Lys	Leu	Arg	Lys	ATG Met 495	AAC Asn	TCT Ser	GAC Asp	CGC Arg	TTC Phe 500	ACA Thr			1534
TAG	CAAA	ACA	cccc	ATTA	GG C	ATTA	TTTC	A TG	TTTT	GATT	TAG	TTTT	AGT	CCAA	TATTTG	1594
GCT	GATA	AGA	TAAT	сстс	cc c	GGGA	AATC	T GA	GAGG	TCTA	TCC	CAGT	CTG	GCAA	ATTCAT	1654
CAG	AGGA	CTC	TTCA	TTGA	AG T	GTTG	TTAC	T GT	GTTG	AACA	TGA	GTTA	CAA	AGGG	AGGACA	1714
TCA	TAAG	AAA	GCTA	ATAG	TT G	GCAT	GTAT	T AT	CACA	TCAA	GCA	TGCA	ATA	ATGT	GCAAAT	1774
TTT	GCAT	TTA	GTTT	TCTG	GC A	TGAT	TTAT	A TA	TGGC	ATAT	TTA	TATT	GAA	TATT	CTGGAA	1834
AAA	TATA	AAT	ATAT	TATA	TT G	AAGT	GGAG	A TA	TTCT	cccc	ATA	ATTT	CTA	ATAT	ATGTAT	1894
TAA	GCCA	AAC	ATGA	GTGG	AT A	GCTT	TCAG	G GC	ACTA	AAAT	AAT	ATAC	ATG	CATA	CATACA	1954
TAC	ATGO	ATA	TGCA	CAGA	CA C	ATAC	ACAC	A CA	TACT	CATA	TAT	'ATAA	AAC	ATAC	CCATAC	2014
AAA	CATA	TAT	ATCI	'AATA	AA A	ATTG	TGAT	G TI	TTGT	TCAA	AAA	AAAA	AAA	AAAA	AACTCG	2074
AG																2076

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile 145 Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val 215 Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser 250 Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His 265 Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met 280 Gln Thr Glu Gln Phe Glu Val Val Ile Leu Glu Gly Ile Val Glu

Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu

315

310

Ser Asp Arg Phe Thr

500



Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Gly 325 330 Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys Glu Glu Glu Met Leu Leu Met Ser 360 Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn 375 Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp 425 Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser 455 Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly 475 470 Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn